

SEQUENCE LISTING

<110> Degussa-Hüls AG, Forschungszentrum Jülich GmbH

<120> Novel nucleotide sequences coding for the cdsA gene

<130> 000009 BT

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<170> PatentIn Ver. 2.1

<210> 1

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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (200)..(1090)

<223> cdsA gene

<220>

<221> RBS

<222> (187)..(195)

<400> 1

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gcaagagtgt ttggaagaat tttttcgaaa atgctggcac catcaacagt gacattgtta 180
gaaacttcaa ggagaaccc atg aat gaa ccg gag caa cat cac cgg tcc atg 232
                Met Asn Glu Pro Glu Gln His His Arg Ser Met
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agg atg ccc aaa ccc aaa aat aat gcg ggt cga gat ctc aaa gct gcc 280
Arg Met Pro Lys Pro Lys Asn Asn Ala Gly Arg Asp Leu Lys Ala Ala
                15          20          25

att gct gtg ggg atc gga ctg ggg gtc ctg gtt ctt ttg ggg att gtc 328
Ile Ala Val Gly Ile Gly Leu Gly Val Leu Val Leu Leu Gly Ile Val
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cta agc cca tgg ggt tgg tac atc ctc gtt gca ggt ttt atg gct gca 376
Leu Ser Pro Trp Gly Trp Tyr Ile Leu Val Ala Gly Phe Met Ala Ala
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gca aca tgg gaa gtt ggt agc aga ctt aaa gaa ggc ggc tat cat ttg 424
Ala Thr Trp Glu Val Gly Ser Arg Leu Lys Glu Gly Gly Tyr His Leu
                60          65          70          75

cca ctg ccg att atg atc atc ggc ggt cag gca atc atc tgg ctg tca 472
Pro Leu Pro Ile Met Ile Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser
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tgg cca ttt ggc acg atg ggc att ttg gcg tct ttt gtg gcc act gtg 520

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Trp	Pro	Phe	Gly 95	Thr	Met	Gly	Ile	Leu	Ala	Ser	Phe	Val	Ala	Thr	Val	
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Leu	Val	Leu	Met	Tyr	Phe	Arg	Ile	Phe	Tyr	Asn	Gly	Thr	Glu	Lys	Glu	
		110					115					120				
gcc	cgc	aac	tat	ttg	agg	gac	acc	tct	gtg	ggc	atc	ttc	gtg	ctc	acc	616
Ala	Arg	Asn	Tyr	Leu	Arg	Asp	Thr	Ser	Val	Gly	Ile	Phe	Val	Leu	Thr	
		125					130				135					
tgg	att	cca	ttg	ttc	gga	agc	ttc	gct	gcg	atg	ctg	tcg	ctg	atg	caa	664
Trp	Ile	Pro	Leu	Phe	Gly	Ser	Phe	Ala	Ala	Met	Leu	Ser	Leu	Met	Gln	
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aac	aat	tcc	atc	ccg	ggt	aca	tat	ttc	att	ttg	acg	ttc	atg	ctg	tgt	712
Asn	Asn	Ser	Ile	Pro	Gly	Thr	Tyr	Phe	Ile	Leu	Thr	Phe	Met	Leu	Cys	
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gtg	atc	gca	tcg	gat	gtg	ggc	ggg	tat	atc	gcg	ggc	gtg	ttc	ttt	gga	760
Val	Ile	Ala	Ser	Asp	Val	Gly	Gly	Tyr	Ile	Ala	Gly	Val	Phe	Phe	Gly	
			175					180					185			
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Ser	His	Pro	Met	Ala	Pro	Leu	Val	Ser	Pro	Lys	Lys	Ser	Trp	Glu	Gly	
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ttt	gcc	ggc	tcc	att	gtc	tta	gga	tcg	gtc	act	ggc	gca	ctc	agt	gtt	856
Phe	Ala	Gly	Ser	Ile	Val	Leu	Gly	Ser	Val	Thr	Gly	Ala	Leu	Ser	Val	
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gcc	cta	gtt	gtg	tgc	gcc	acg	ttg	ggt	gac	ttg	gtt	gag	tcg	cag	ttc	952
Ala	Leu	Val	Val	Cys	Ala	Thr	Leu	Gly	Asp	Leu	Val	Glu	Ser	Gln	Phe	
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Lys	Arg	Asp	Leu	Gly	Ile	Lys	Asp	Met	Ser	Asn	Leu	Leu	Pro	Gly	His	
			255					260					265			
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Gly	Gly	Leu	Met	Asp	Arg	Leu	Asp	Gly	Met	Leu	Pro	Ala	Ala	Met	Val	
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acg	tgg	ttg	atc	ctg	agt	gtg	atc	agc	agc	tcg	tat	ccg	tcg			1090
Thr	Trp	Leu	Ile	Leu	Ser	Val	Ile	Ser	Ser	Ser	Tyr	Pro	Ser			
		285				290					295					
taaagcttg gccagcttta agttcaaaaa acttgaaagg cgctgaggtg cataacgtgt																1150
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<213> Corynebacterium glutamicum

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35 40 45
Trp Tyr Ile Leu Val Ala Gly Phe Met Ala Ala Ala Thr Trp Glu Val
50 55 60
Gly Ser Arg Leu Lys Glu Gly Gly Tyr His Leu Pro Leu Pro Ile Met
65 70 75 80
Ile Ile Gly Gly Gln Ala Ile Ile Trp Leu Ser Trp Pro Phe Gly Thr
85 90 95
Met Gly Ile Leu Ala Ser Phe Val Ala Thr Val Leu Val Leu Met Tyr
100 105 110
Phe Arg Ile Phe Tyr Asn Gly Thr Glu Lys Glu Ala Arg Asn Tyr Leu
115 120 125
Arg Asp Thr Ser Val Gly Ile Phe Val Leu Thr Trp Ile Pro Leu Phe
130 135 140
Gly Ser Phe Ala Ala Met Leu Ser Leu Met Gln Asn Asn Ser Ile Pro
145 150 155 160
Gly Thr Tyr Phe Ile Leu Thr Phe Met Leu Cys Val Ile Ala Ser Asp
165 170 175
Val Gly Gly Tyr Ile Ala Gly Val Phe Phe Gly Ser His Pro Met Ala
180 185 190
Pro Leu Val Ser Pro Lys Lys Ser Trp Glu Gly Phe Ala Gly Ser Ile
195 200 205
Val Leu Gly Ser Val Thr Gly Ala Leu Ser Val His Phe Leu Leu Asp
210 215 220
His His Trp Trp Met Gly Val Ile Leu Gly Cys Ala Leu Val Val Cys
225 230 235 240
Ala Thr Leu Gly Asp Leu Val Glu Ser Gln Phe Lys Arg Asp Leu Gly
245 250 255
Ile Lys Asp Met Ser Asn Leu Leu Pro Gly His Gly Gly Leu Met Asp
260 265 270
Arg Leu Asp Gly Met Leu Pro Ala Ala Met Val Thr Trp Leu Ile Leu
275 280 285
Ser Val Ile Ser Ser Ser Tyr Pro Ser
290 295